

Q. Nguyen

#10

12-22-00

1632

P.2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/462,517

DATE: 11/21/2000

TIME: 11:52:46

Input Set : A:\sequence

Output Set: N:\CRF3\11212000\I462517.raw

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supp.

3 <110> APPLICANT: Aurora Biosciences Corporation
4 Zucker, Charles
5 Mendlein, John
6 Sun, Yumei
7 Tsunoda, Susan
8 Sierralta, Jimena
10 <120> TITLE OF INVENTION: Compositions And Methods For Identifying Modulators and Transducisomes
12 <130> FILE REFERENCE: AU01210-1
14 <140> CURRENT APPLICATION NUMBER: 09/462,517
15 <141> CURRENT FILING DATE: 2000-05-18
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 674
23 <212> TYPE: PRT
24 <213> ORGANISM: Drosophila melanogaster
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29 1 5 10 15
31 Met Val Thr Leu Asp Lys Thr Gly Lys Lys Ser Phe Gly Ile Cys Ile
32 20 25 30
34 Val Arg Gly Glu Val Lys Asp Ser Pro Asn Thr Lys Thr Gly Ile
35 35 40 45
37 Phe Ile Lys Gly Ile Val Pro Asp Ser Pro Ala His Leu Cys Gly Arg
38 50 55 60
40 Leu Lys Val Gly Asp Arg Ile Leu Ser Leu Asn Gly Lys Asp Val Arg
41 65 70 75 80
43 Asn Ser Thr Glu Gln Ala Val Ile Asp Leu Ile Lys Glu Ala Asp Phe
44 85 90 95
46 Lys Ile Glu Leu Glu Ile Gln Thr Phe Asp Lys Ser Asp Glu Gln Gln
47 100 105 110
49 Ala Lys Ser Asp Pro Arg Ser Asn Gly Tyr Met Gln Ala Lys Asn Lys
50 115 120 125
52 Phe Asn Gln Glu Gln Thr Thr Asn Asn Asn Ala Ser Gly Gly Gln Gly
53 130 135 140
55 Met Gly Gln Gly Gln Gly Gln Gly Met Ala Gly Met Asn Arg
56 145 150 155 160
58 Gln Gln Ser Met Gln Lys Arg Asn Thr Thr Phe Thr Ala Ser Met Arg
59 165 170 175
61 Gln Lys His Ser Asn Tyr Ala Asp Glu Asp Asp Glu Asp Thr Arg Asp
62 180 185 190
64 Met Thr Gly Arg Ile Arg Thr Glu Ala Gly Tyr Glu Ile Asp Arg Ala
65 195 200 205
67 Ser Ala Gly Asn Cys Lys Leu Asn Lys Gln Glu Lys Asp Arg Asp Lys
68 210 215 220
70 Glu Gln Glu Asp Glu Phe Gly Tyr Thr Met Ala Lys Ile Asn Lys Arg
71 225 230 235 240

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73 Tyr Asn Met Met Lys Asp Leu Arg Arg Ile Glu Val Gln Arg Asp Ala
74                               245                               250                               255
76 Ser Lys Pro Leu Gly Leu Ala Leu Ala Gly His Lys Asp Arg Gln Lys
77                               260                               265                               270
79 Met Ala Cys Phe Val Ala Gly Val Asp Pro Asn Gly Ala Leu Gly Ser
80                               275                               280                               285
82 Val Asp Ile Lys Pro Gly Asp Glu Ile Val Glu Val Asn Gly Asn Val
83                               290                               295                               300
85 Leu Lys Asn Arg Cys His Leu Asn Ala Ser Ala Val Phe Lys Asn Val
86 305                               310                               315                               320
88 Asp Gly Asp Lys Leu Val Met Ile Thr Ser Arg Arg Lys Pro Asn Asp
89                               325                               330                               335
91 Glu Gly Met Cys Val Lys Pro Ile Lys Lys Phe Pro Thr Ala Ser Asp
92                               340                               345                               350
94 Glu Thr Lys Phe Ile Phe Asp Gln Phe Pro Lys Ala Arg Thr Val Gln
95                               355                               360                               365
97 Val Arg Lys Glu Gly Phe Leu Gly Ile Met Val Ile Tyr Gly Lys His
98                               370                               375                               380
100 Ala Glu Val Gly Ser Gly Ile Phe Ile Ser Asp Leu Arg Glu Gly Ser
101 385                               390                               395                               400
103 Asn Ala Glu Leu Ala Gly Val Lys Val Gly Asp Met Leu Leu Ala Val
104                               405                               410                               415
106 Asn Gln Asp Val Thr Leu Glu Ser Asn Tyr Asp Asp Ala Thr Gly Leu
107                               420                               425                               430
109 Leu Lys Arg Ala Glu Gly Val Val Thr Met Ile Leu Leu Thr Leu Lys
110                               435                               440                               445
112 Ser Glu Glu Ala Ile Lys Ala Glu Lys Ala Ala Glu Glu Lys Lys Lys
113                               450                               455                               460
115 Glu Glu Ala Lys Lys Glu Glu Glu Lys Pro Gln Glu Pro Ala Thr Ala
116 465                               470                               475                               480
118 Glu Ile Lys Pro Asn Lys Lys Ile Leu Ile Glu Leu Lys Val Glu Lys
119                               485                               490                               495
121 Lys Pro Met Gly Cys His Arg Leu Arg Arg Gln Lys Gln Pro Cys His
122                               500                               505                               510
124 Asp Trp Leu Cys Asn His Pro Arg Leu Ser Gly Gly Gln Val Ala Ala
125                               515                               520                               525
127 Asp Lys Arg Leu Lys Ile Phe Asp His Ile Cys Asp Ile Asn Gly Thr
128                               530                               535                               540
130 Pro Ile His Val Gly Ser Met Thr Thr Leu Lys Val His Gln Leu Phe
131 545                               550                               555                               560
133 His Thr Thr Tyr Glu Lys Ala Val Thr Leu Thr Val Phe Arg Ala Asp
134                               565                               570                               575
136 Pro Pro Glu Leu Glu Lys Phe Asn Val Asp Leu Met Lys Lys Ala Gly
137                               580                               585                               590
139 Lys Glu Leu Gly Leu Ser Leu Ser Pro Asn Glu Ile Gly Cys Thr Ile
140                               595                               600                               605
142 Ala Asp Leu Ile Gln Gly Gln Tyr Pro Glu Ile Asp Ser Lys Leu Gln
143                               610                               615                               620
145 Arg Gly Asp Ile Ile Thr Lys Phe Asn Gly Asp Ala Leu Glu Gly Leu

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146 625          630          635          640
148 Pro Phe Gln Val Cys Tyr Ala Leu Phe Lys Gly Ala Asn Gly Lys Val
149          645          650          655
151 Ser Met Glu Val Thr Arg Pro Lys Pro Thr Leu Arg Thr Glu Ala Pro
152          660          665          670
154 Lys Ala
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 2059
159 <212> TYPE: DNA
160 <213> ORGANISM: Drosophila melanogaster
162 <400> SEQUENCE: 2
163 atggttcaqt tcctgggcaa acagggcacc qcggttgagc tcattcacat ggtgacctg 60
165 gacaagacyg gcaagaagtc ctctggcacc tgcatagtgc qcggcgaggt gaaqgattcg 120
167 cccaacacca agacaaccgg catcttcacc aagggcattg tgcccgacag tcccgcgcac 180
169 ctggtgtggtc gcctaaaagt tggcgatcgg atcctctcgc tcaacggaaa ggaatgtgcgc 240
171 aactccaccg aacaggcggt catcgatctc atcaaggagg cggacttcaa gatcgagctg 300
173 gagattcaga ccttcgacaa gagcgatgag cagcaggcca agtcagatcc gcgagacaa 360
175 ggctacatgc aggccaaaga caagtccaat caggagcaga ccaccaacaa caatgcgtcc 420
177 ggaggtcagg gaatggggca aggtcagggt cagggtcagg gaatggctgg catgaaccgg 480
179 cagcaatcga tgcagaagcy gaataccaca ttacggcct cgaatgcgtc gaagcatagt 540
181 aactacgcgc acgaggatga cgaaggaccc cgggacatga ccggtcgcat tcgcacggag 600
183 qcggtgttatg agatcgatcg agcctccgcc ggtaattgca aacttaataa gcaggaaaaa 660
185 gatcgcgaca aggagcagga agatgaatct ggctacacga tggctaagat caacaagcgg 720
187 tacaacatga tgaaggatct gcgcagatc gaggtccaga gggagccag caagccactg 780
189 qgactcgcac tcgctggcca caaagaccgc cagaagatgg cctgctttgt tgcgggtgtg 840
191 gatcccaacg gagcattggg cagcgtggac attaagccgg gcgacgagat cgtcgaggtc 900
193 aacggcaatg tgcctaaaga tcgctgccac ttgaacgcct ccgctgtgtt caagagcgtg 960
195 gatggggata agctcgtgat gatcacctcg cgaagcaagc ccaacgatga gggcatgtgc 1020
197 gtcaagccca tcaaaaagtt cccacccgcy tctgatgaga ctaagtttat ctccgaccag 1080
199 ttteccaagg cgcgcacggt gcagggtgcgc aaggaggggt cctgggcacc atggtcatct 1140
201 atggcaagca cgtctgaggt ggcaagtgga ttttcacctc ggatctgaga gagggatcga 1200
203 atgcccaggt ggcggcgctg aaagtggggc acatgctgct ggccttaat caggatgtaa 1260
205 cactggaatc caactacgat gatgctactg gaactgctaa acytcgcgag ggcgtagtga 1320
207 ccatgattct attgactctc aagagcgagg aggcgataaa ggcctgagaag gcagcggaag 1380
209 agaaaaagaa ggaggaggcc aagaaaaggg aggaaaagcc acaggaaacc gccacagccg 1440
211 agatcaagcc gaacaaaaag atactcattg agttgaaggt ggaaaaagaa ccaatggggc 1500
213 tcactgtctg cggcggaag aaacaaccat tcacgactgg ctgtgtaate accacggttt 1560
215 atccygaggg acaagtggca gccgacaagc gccccaagat ctttgaccac atttgtgata 1620
217 taaatgggtac gccaatccac gtgggatcca tgacgacact gaaggtccat cagttattcc 1680
219 acaccacata cgagaaggcg gtcacctaa cggctctccg cgtgatctct ccggaaactg 1740
221 aaaagtttaa cgttgacctt atgaaaaaag caggcaagga gctgggacct tcgctgtctc 1800
223 ccaacgaaat tggatgcacc atcgcggaat tgattcaagg acaataccgg gagattgaca 1860
225 gcaaaactga gcgcggcgat attatacca attcaatggc gatgccttgg agggctcttc 1920
227 gttccagggt tgcctacgct tgttcaaggg agccaacggc aaggtatcga tggaaagtgc 1980
229 acgacccaag ccactctac gtacggaggc acccaaggcc tagagacgat cctcattctc 2040
231 ctctccgtag cgaagcagt 2059
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 93
236 <212> TYPE: PRT

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237 <213> ORGANISM: artificial
239 <220> FEATURE:
240 <223> OTHER INFORMATION: PSD-1
242 <400> SEQUENCE: 3
244 Met Glu Tyr Glu Glu Ile Thr Leu Glu Arg Gly Asn Ser Gly Leu Gly
245 1 5 10 15
247 Phe Ser Ile Ala Gly Gly Thr Asp Asn Pro His Ile Gly Asp Asp Pro
248 20 25 30
250 Ser Ile Phe Ile Thr Lys Ile Ile Pro Gly Gly Ala Ala Ala Gln Asp
251 35 40 45
253 Gly Arg Leu Arg Val Asn Asp Ser Ile Leu Phe Val Asn Glu Val Asp
254 50 55 60
256 Val Arg Glu Val Thr His Ser Ala Ala Val Glu Ala Leu Lys Glu Ala
257 65 70 75 80
259 Gly Ser Ile Val Arg Leu Tyr Val Met Arg Arg Lys Pro
260 85 90
262 <210> SEQ ID NO: 4
263 <211> LENGTH: 93
264 <212> TYPE: PRT
265 <213> ORGANISM: Artificial
267 <220> FEATURE:
268 <223> OTHER INFORMATION: PSD95-2
270 <400> SEQUENCE: 4
272 Glu Lys Val Met Glu Ile Lys Leu Ile Lys Gly Pro Lys Gly Leu Gly
273 1 5 10 15
275 Phe Ser Ile Ala Gly Gly Val Gly Asn Gln His Ile Pro Gly Asp Asn
276 20 25 30
278 Ser Ile Tyr Val Thr Lys Ile Ile Glu Gly Gly Ala Ala His Lys Asp
279 35 40 45
281 Gly Arg Leu Gln Ile Gly Asp Lys Ile Leu Ala Val Asn Ser Val Gly
282 50 55 60
284 Leu Glu Asp Val Met His Glu Asp Ala Val Ala Ala Leu Lys Asn Thr
285 65 70 75 80
287 Tyr Asp Val Val Tyr Leu Lys Val Ala Lys Pro Ser Asn
288 85 90
290 <210> SEQ ID NO: 5
291 <211> LENGTH: 87
292 <212> TYPE: PRT
293 <213> ORGANISM: artificial
295 <220> FEATURE:
296 <223> OTHER INFORMATION: PSD95-3
298 <400> SEQUENCE: 5
300 Arg Glu Pro Arg Arg Ile Val Ile His Arg Gly Ser Thr Gly Leu Gly
301 1 5 10 15
303 Phe Asn Ile Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe
304 20 25 30
306 Ile Leu Ala Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly
307 35 40 45
309 Asp Gln Ile Leu Ser Val Asn Gly Val Asp Leu Arg Asn Ala Ser His

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310      50      55      60
312 Glu Gln Ala Ala Ile Ala Leu Lys Asn Ala Gly Gln Thr Val Thr Ile
313 65      70      75      80
315 Ile Ala Gln Tyr Lys Pro Glu
316      85
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 87
320 <212> TYPE: PRT
321 <213> ORGANISM: artificial
323 <220> FEATURE:
324 <223> OTHER INFORMATION: dlq-3
326 <400> SEQUENCE: 6
328 Arg Glu Pro Arg Thr Ile Thr Ile Gln Lys Gly Pro Gln Gly Leu Gly
329 1      5      10      15
331 Phe Asn Ile Val Gly Gly Glu Asp Gly Gln Gly Ile Tyr Val Ser Phe
332      20      25      30
334 Ile Leu Ala Gly Gly Pro Ala Asp Leu Gly Ser Glu Leu Lys Arg Gly
335      35      40      45
337 Asp Gln Leu Leu Ser Val Asn Asn Val Asn Leu Thr His Ala Thr His
338      50      55      60
340 Glu Glu Ala Ala Gln Ala Leu Lys Thr Ser Gly Gly Val Val Thr Leu
341 65      70      75      80
343 Leu Ala Gln Tyr Arg Pro Glu
344      85
346 <210> SEQ ID NO: 7
347 <211> LENGTH: 88
348 <212> TYPE: PRT
349 <213> ORGANISM: artificial
351 <220> FEATURE:
352 <223> OTHER INFORMATION: nNOS
354 <400> SEQUENCE: 7
356 Pro Asn Val Ile Ser Val Arg Leu Phe Lys Arg Lys Val Gly Gly Leu
357 1      5      10      15
359 Gly Phe Leu Val Lys Glu Arg Val Ser Lys Pro Pro Val Ile Ile Ser
360      20      25      30
362 Asp Leu Ile Arg Gly Gly Ala Ala Glu Gln Ser Gly Leu Ile Gln Ala
363      35      40      45
365 Gly Asp Ile Ile Leu Ala Val Asn Asp Arg Pro Leu Val Asp Leu Ser
366      50      55      60
368 Tyr Asp Ser Ala Leu Glu Val Leu Arg Gly Ile Ala Ser Glu Thr His
369 65      70      75      80
371 Val Val Leu Ile Leu Arg Gly Pro
372      85
374 <210> SEQ ID NO: 8
375 <211> LENGTH: 88
376 <212> TYPE: PRT
377 <213> ORGANISM: artificial
379 <220> FEATURE:
380 <223> OTHER INFORMATION: inad-3

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FTI!

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 11/21/2000
PATENT APPLICATION: US/09/462,517 TIME: 11:52:47

Input Set : A:\sequence
Output Set: N:\CRF3\11212000\I462517.raw

L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

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